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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Fri May 25 11:38:56 EDT 2007

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Application No: 10511719 Version No: 2.0

Input Set:

Output Set:

Started: 2007-05-18 10:55:18.304
Finished: 2007-05-18 10:55:19.121
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 817 ms
Total Warnings: 7
Total Errors: 2
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 249	Order Sequence Error <213> -> <213>; Expected Mandatory Tag: <400> in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> REGEN Biotech. Inc.

<120> The method for measuring the amount of BetaIG-H3 protein and diagnostic kit using the same

<130> 2fpo-10-14

<160> 12

<170> KopatentIn 1.71

<210> 1

<211> 683

<212> PRT

<213> Homo sapiens

<400> 1

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Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu
20 25 30

Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
100 105 110

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
130 135 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
165 170 175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
180 185 190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
195 200 205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala		
210	215	220
Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr		
225	230	235 240
Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu		
	245	250 255
Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn		
	260	265 270
Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile		
	275	280 285
Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg		
	290	295 300
Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala		
305	310	315 320
Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu		
	325	330 335
Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile		
	340	345 350
Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp		
	355	360 365
Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala		
	370	375 380
Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu		
385	390	395 400
Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu		
	405	410 415
Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg		
	420	425 430
Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr		
	435	440 445
Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg		
	450	455 460
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala		
465	470	475 480
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg		
	485	490 495
Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp		
	500	505 510

Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
 515 520 525
 Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
 530 535 540
 Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
 545 550 555 560
 Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
 565 570 575
 Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
 580 585 590
 Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
 595 600 605
 Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
 610 615 620
 Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
 625 630 635 640
 Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
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<210> 2
 <211> 2691
 <212> DNA
 <213> Homo sapiens

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aggcttttat ggggccctgt ccaggtagaa aagaaatggg atgtagagct tagatttccc 2640

tattgtgaca gagccatggg gtgtttgtaa taataaaacc aaagaaacat a 2691

<210> 3

<211> 585

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(585)

<223> 69 to 653 amino acid sequence of human ID No.1

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20 25 30

Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr

35 40 45

Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met

50 55 60

Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp

65 70 75 80

Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn

85 90 95

Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val

100 105 110

Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln

115 120 125

Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val

130 135 140

Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val

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Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln						
	165		170		175	
Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val						
	180		185		190	
Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr						
	195		200		205	
Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr						
	210		215		220	
Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn						
225		230		235		240
Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly						
	245		250		255	
Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser						
	260		265		270	
Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp						
	275		280		285	
Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile						
	290		295		300	
Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val						
305		310		315		320
Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu						
	325		330		335	
Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe						
	340		345		350	
Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg						
	355		360		365	
Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly						
	370		375		380	
Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr						
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Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys						
	405		410		415	
Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro						
	420		425		430	
Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser						
	435		440		445	
Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn						

450	455	460
Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg		
465	470	475 480
Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu		
485	490	495
Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser		
500	505	510
Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys		
515	520	525
Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro		
530	535	540
Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile		
545	550	555 560
Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp		
565	570	575
Glu Leu Ala Asp Ser Ala Leu Glu Ile		
580	585	

<210> 4
 <211> 1857
 <212> DNA
 <213> Mouse Intracisternal A-particle

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gagtgtgtgc ctggatatga aaagggtcca ggagagaaag gttgcccagc agctcttcg	240
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gatgagctca agcacggcat gaccctcacc tccatgtacc agaattccaa catccagatc	540
catcactatc ccaatgggat tgtaactgtt aactgtgccc ggctgtgaa ggctgaccac	600
catgcgacca acggcgtggt gcatctcatt gacaagggtca tttccaccat caccaacaac	660
atccagcaga tcattgaaat cgaggacacc tttgagacac ttcgggccgc cgtggctgca	720

tcaggactca ataccgtgct ggagggcgac ggccagttca cactcttggc cccaaccaac	780
gaggcctttg agaagatccc tgccgagacc ttgaaccgca tcctgggtga ccagaggca	840
ctgagagacc tgctaaacaa ccacatcctg aagtcagcca tgtgtgctga ggccattgta	900
gctggaatgt ccatggagac cctggggggc accacactgg aggtgggtg cagtggggac	960
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ctgcgagtct ttgtttatcg aaatagcctc tgcattgaaa acagctgcat tgctgcccat	1380
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gggacagtta tggatgtcct gaaggagac aatcgtttta gcatgctggt ggccgccatc	1500
cagtctgcag gactcatgga gatcctcaac cgggaagggg tctacactgt ttttgctccc	1560
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<210> 5
 <211> 609
 <212> PRT
 <213> Mouse Intracisternal A-particle

 <220>
 <221> PEPTIDE
 <222> (1)..(609)
 <223> 23 to 641 amino acid sequence of mouse

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Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn Cys Lys Gln Trp Tyr Gln
35 40 45

Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys Cys Pro
50 55 60

Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala Leu Pro
65 70 75 80

Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr Thr Thr
85 90 95

Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met Glu Gly
100 105 110

Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp Ala Ser
115 120 125

Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn Ile Glu
130 135 140

Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val Leu Thr
145 150 155 160

Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln Asn Ser
165 170 175

Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val Asn Cys
180 185 190

Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val Val His
195 200 205

Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln Gln Ile
210 215 220

Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Va